

Supplement- Predicting signalling pathway features by nested effect modelling, demonstrated on Wnt signalling in HCT116 cells

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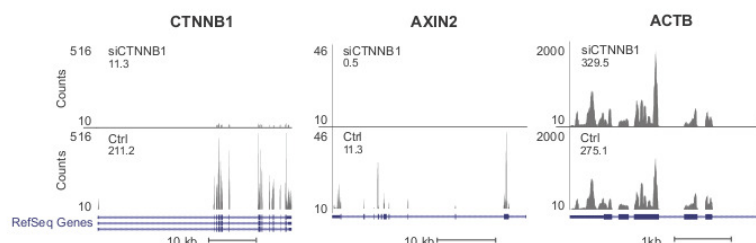
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S1 Fig.



Sequence reads. Example plots of the distribution of reads for selected genes based on RNAseq experiments using *CTNNB1* (β -catenin) in the upper panels and control siRNAs in the lower panels. *AXIN2* is a target gene of canonical Wnt signalling, *ACTB* is an unrelated control. Sequence reads were mapped to the genome and the frequency at each base is plotted as height of the bars.